

D2
conclude
which encodes a TADG-14 protein having the amino acid sequence shown
in SEQ ID No. 7.

Please amend claim 11 as follows:

D3
AFB
11. (amended) A method of detecting expression of the protein encoded by the DNA of claim 1, comprising the steps of:

(a) contacting mRNA obtained from a cell with a labeled hybridization probe corresponding to the open reading frame of said DNA; and

(b) detecting hybridization of said probe with said mRNA.

REMARKS

The 35 USC §112 Rejections

Claims 1, 4, 6-8, and 11 remain rejected under 35 USC §112, first paragraph as being non-enabled. This rejection is respectfully traversed.

Polymorphisms in the amino acid sequence of proteins are a common phenomenon, and it is likely that TADG-14 proteins exist which vary at a few amino acid positions. Therefore, claim 1 has been amended. Therefore, the Applicants respectfully request

that the 35 USC §112, first paragraph rejection of claims 1, 4, 6-8, and 11 be withdrawn.

Claims 1, 4, 6-8, and 11 stand rejected under 35 USC §112 as unpatentable because a protein cannot be encoded by the polynucleotide that hybridizes to the coding strand unless the gene is palindromic. This rejection is respectfully traversed.

With respect to parts b) and c) of claim 1, except in few viruses, DNA is generally double stranded. As the TADG-14 gene described here is a human, and thus a eukaryotic gene, the isolated gene of part a) of claim 1 will contain both strands. Thus, DNA which hybridizes to part a) can encode a protein. The Applicants respectfully request that the 35 USC §112 rejection of claims 1, 4, 6-8, and 11 over this issue be withdrawn.

Claim 11 is rejected under 35 USC §112 as unpatentable because the specification states that hybridization probes were used to detect mRNA transcripts encoding TADG-14 but was silent as to which probes were useful. This rejection is respectfully traversed.

Claim 11 has been amended to state the hybridization probe should be derived from the open reading frame of the DNA of

claim 1. This would be obvious to one skilled in the art and thus there is no need for the specification to specifically state this. Therefore, the Applicants respectfully request that the 35 USC §112 rejection of claim 11 be withdrawn.

Claims 1, 4, 6-8, and 11 remains rejected under 35 USC §112, second paragraph as unpatentable because claim 1 recites DNA molecules having 80% (now amended to 95%) sequence identity but does not specify the percentage algorithm to use and the parameters to set in the algorithm. This rejection is respectfully traversed.

Claim 1 has been amended. Applicants respectfully request that this 35 USC §112, second paragraph rejection of claims 1, 4, 6-8, and 11 be withdrawn.

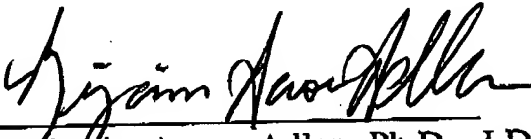
Claims 1, 4, 6-8, and 11 are rejected under 35 USC §112, second paragraph as unpatentable because the specification does not reasonably define "medium or high stringency conditions." This rejection is respectfully traversed.

Claims 1, 4, 6-8, and 11 have been amended. Accordingly, Applicants respectfully request that this 35 USC §112, second paragraph rejection of claims 1, 4, 6-8, and 11 be withdrawn.

This is intended to be a complete response to the Final Office Action mailed May 17, 1999. If any issues remain outstanding, the Examiner is respectfully requested to telephone the undersigned attorney of record for immediate resolution.

Respectfully submitted,

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